SEQUENCE LISTING

<110> Gao, Zeren

<120> Murine Cytokine Receptor

<130> 00-46

<160> 8

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 2256
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (197)...(2218)

<400> 1

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caggggcgag gggtctgccc ccccttgggg gggcaggacg gggcctcagg cctgggtgct    180
gtccggcacc tggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca ctg    232
                  Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu
                   1               5                  10

ggc cga aac cct gtg gtc gtc tct ctg gag aga ctg atg gag cct cag      280
Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln
          15                  20                  25

gac act gca cgc tgc tct cta ggc ctc tcc tgc cac ctc tgg gat ggt      328
Asp Thr Ala Arg Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly
      30                  35                  40

gac gtg ctc tgc ctg cct gga agc ctc cag tct gcc cca ggc cct gtg      376
Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val
  45                  50                  55                  60

cta gtg cct acc cgc ctg cag acg gag ctg gtg ctg agg tgt cca cag      424
Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln
                  65                  70                  75

aag aca gat tgc gcc ctc cgt gtc cgt gtg gtg gtc cac ttg gcc gtg      472
Lys Thr Asp Cys Ala Leu Arg Val Arg Val Val Val His Leu Ala Val
              80                  85                  90

cat ggg cac tgg gca gag cct gaa gaa gct gga aag tct gat tca gaa      520
His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu
          95                  100                 105

ctc cag gag tct agg aac gcc tct ctc cag gcc cag gtg gtg ctc tcc      568
Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
      110                 115                 120

ttc cag gcc tac ccc atc gcc cgc tgt gcc ctg ctg gag gtc cag gtg      616
Phe Gln Ala Tyr Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val
125                 130                 135                 140
```

```
ccc gct gac ctg gtg cag cct ggt cag tcc gtg ggt tct gcg gta ttt      664
Pro Ala Asp Leu Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe
                145                 150                 155

gac tgt ttc gag gct agt ctt ggg gct gag gta cag atc tgg tcc tac      712
Asp Cys Phe Glu Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr
            160                 165                 170

acg aag ccc agg tac cag aaa gag ctc aac ctc aca cag cag ctg cct      760
Thr Lys Pro Arg Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro
        175                 180                 185

gat ggt gac aat gtc ctt ctg aca ctg gat gtc tct gag gag cag gac      808
Asp Gly Asp Asn Val Leu Leu Thr Leu Asp Val Ser Glu Glu Gln Asp
    190                 195                 200

ttt agc ttc tta ctg tac ctg cgt cca gtc ccg gat gct ctc aaa tcc      856
Phe Ser Phe Leu Leu Tyr Leu Arg Pro Val Pro Asp Ala Leu Lys Ser
205                 210                 215                 220

ttg tgg tac aaa aac ctg act gga cct cag aac att act tta aac cac      904
Leu Trp Tyr Lys Asn Leu Thr Gly Pro Gln Asn Ile Thr Leu Asn His
                225                 230                 235

aca gac ctg gtt ccc tgc ctc tgc att cag gtg tgg tcg cta gag cca      952
Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp Ser Leu Glu Pro
            240                 245                 250

gac tct gag agg gtc gaa ttc tgc ccc ttc cgg gaa gat ccc ggt gca     1000
Asp Ser Glu Arg Val Glu Phe Cys Pro Phe Arg Glu Asp Pro Gly Ala
        255                 260                 265

cac agg aac ctc tgg cac ata gcc agg ctg cgg gta ctg tcc cca ggg     1048
His Arg Asn Leu Trp His Ile Ala Arg Leu Arg Val Leu Ser Pro Gly
    270                 275                 280

gta tgg cag cta gat gcg cct tgc tgt ctg ccg ggc aag gta aca ctg     1096
Val Trp Gln Leu Asp Ala Pro Cys Cys Leu Pro Gly Lys Val Thr Leu
285                 290                 295                 300

tgc tgg cag gca cca gac cag agt ccc tgc cag cca ctt gtg cca cca     1144
Cys Trp Gln Ala Pro Asp Gln Ser Pro Cys Gln Pro Leu Val Pro Pro
                305                 310                 315

gtg ccc cag aag aac gcc act gtg aat gag cca caa gat ttc cag ttg     1192
Val Pro Gln Lys Asn Ala Thr Val Asn Glu Pro Gln Asp Phe Gln Leu
            320                 325                 330

gtg gca ggc cac ccc aac ctc tgt gtc cag gtg agc acc tgg gag aag     1240
Val Ala Gly His Pro Asn Leu Cys Val Gln Val Ser Thr Trp Glu Lys
        335                 340                 345

gtt cag ctg caa gcg tgc tcg tgg gct gac tcc ttg ggg ccc ttc aag     1288
Val Gln Leu Gln Ala Cys Ser Trp Ala Asp Ser Leu Gly Pro Phe Lys
    350                 355                 360

gat gat atg ctg tta gtg gag atg aaa acc ggc ctc aac aac aca tca     1336
Asp Asp Met Leu Leu Val Glu Met Lys Thr Gly Leu Asn Asn Thr Ser
365                 370                 375                 380

gtc tgt gcc ttg gaa ccc agt ggc tgt aca cca ctg ccc agc atg gcc     1384
```

```
Val Cys Ala Leu Glu Pro Ser Gly Cys Thr Pro Leu Pro Ser Met Ala
                385                 390                 395

tcc acg aga gct gct cgc ctg gga gag gag ttg ctg caa gac ttc cga     1432
Ser Thr Arg Ala Ala Arg Leu Gly Glu Glu Leu Leu Gln Asp Phe Arg
            400                 405                 410

tca cac cag tgt atg cag ctg tgg aac gat gac aac atg gga tcg cta     1480
Ser His Gln Cys Met Gln Leu Trp Asn Asp Asp Asn Met Gly Ser Leu
        415                 420                 425

tgg gcc tgc ccc atg gac aag tac atc cac agg cgc tgg gtc cta gta     1528
Trp Ala Cys Pro Met Asp Lys Tyr Ile His Arg Arg Trp Val Leu Val
    430                 435                 440

tgg ctg gcc tgc cta ctc ttg gct gcg gcg ctt ttc ttc ttc ctc ctt     1576
Trp Leu Ala Cys Leu Leu Leu Ala Ala Ala Leu Phe Phe Phe Leu Leu
445                 450                 455                 460

cta aaa aag gac cgc agg aaa gcg gcc cgt ggc tcc cgc acg gcc ttg     1624
Leu Lys Lys Asp Arg Arg Lys Ala Ala Arg Gly Ser Arg Thr Ala Leu
                465                 470                 475

ctc ctc cac tcc gcc gac gga gcg ggc tac gag cgt ctg gtg gga gca     1672
Leu Leu His Ser Ala Asp Gly Ala Gly Tyr Glu Arg Leu Val Gly Ala
            480                 485                 490

ctg gcg tcc gcg ttg agc cag atg cca ctg cgc gtg gcc gtg gac ctg     1720
Leu Ala Ser Ala Leu Ser Gln Met Pro Leu Arg Val Ala Val Asp Leu
        495                 500                 505

tgg agc cgc cgc gag ctg agc gcg cac gga gcc cta gcc tgg ttc cac     1768
Trp Ser Arg Arg Glu Leu Ser Ala His Gly Ala Leu Ala Trp Phe His
    510                 515                 520

cac cag cga cgc cgt atc ctg cag gag ggt ggc gtg gta atc ctt ctc     1816
His Gln Arg Arg Arg Ile Leu Gln Glu Gly Gly Val Val Ile Leu Leu
525                 530                 535                 540

ttc tcg ccc gcg gcc gtg gcg cag tgt cag cag tgg ctg cag ctc cag     1864
Phe Ser Pro Ala Ala Val Ala Gln Cys Gln Gln Trp Leu Gln Leu Gln
                545                 550                 555

aca gtg gag ccc ggg ccg cat gac gcc ctc gcc gcc tgg ctc agc tgc     1912
Thr Val Glu Pro Gly Pro His Asp Ala Leu Ala Ala Trp Leu Ser Cys
            560                 565                 570

gtg cta ccc gat ttc ctg caa ggc cgg gcg acc ggc cgc tac gtc ggg     1960
Val Leu Pro Asp Phe Leu Gln Gly Arg Ala Thr Gly Arg Tyr Val Gly
        575                 580                 585

gtc tac ttc gac ggg ctg ctg cac cca gac tct gtg ccc tcc ccg ttc     2008
Val Tyr Phe Asp Gly Leu Leu His Pro Asp Ser Val Pro Ser Pro Phe
    590                 595                 600

cgc gtc gcc ccg ctc ttc tcc ctg ccc acg cag ctg ccg gct ttc ctg     2056
Arg Val Ala Pro Leu Phe Ser Leu Pro Thr Gln Leu Pro Ala Phe Leu
605                 610                 615                 620

gat gca ctg cag gga ggc tgc tcc act tcc gcg ggg cga ccc gcg gac     2104
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```
Asp Ala Leu Gln Gly Gly Cys Ser Thr Ser Ala Gly Arg Pro Ala Asp
                625                 630                 635

cgg gtg gaa cga gtg acc cag gcg ctg cgg tcc gcc ctg gac agc tgt      2152
Arg Val Glu Arg Val Thr Gln Ala Leu Arg Ser Ala Leu Asp Ser Cys
            640                 645                 650

act tct agc tcg gaa gcc cca ggc tgc tgc gag gaa tgg gac ctg gga      2200
Thr Ser Ser Ser Glu Ala Pro Gly Cys Cys Glu Glu Trp Asp Leu Gly
        655                 660                 665

ccc tgc act aca cta gaa taaaagccga tacagtattc ctaaaaaaaa             2248
Pro Cys Thr Thr Leu Glu
    670

aaaaaaaa                                                             2256

      <210> 2
      <211> 674
      <212> PRT
      <213> mouse

      <400> 2
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 1               5                  10                  15
Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln Asp Thr Ala Arg
            20                  25                  30
Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly Asp Val Leu Cys
        35                  40                  45
Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val Leu Val Pro Thr
    50                  55                  60
Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln Lys Thr Asp Cys
65                  70                  75                  80
Ala Leu Arg Val Arg Val Val Val His Leu Ala Val His Gly His Trp
                85                  90                  95
Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu Leu Gln Glu Ser
            100                 105                 110
Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr
        115                 120                 125
Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val Pro Ala Asp Leu
    130                 135                 140
Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe Asp Cys Phe Glu
145                 150                 155                 160
Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr Thr Lys Pro Arg
                165                 170                 175
Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro Asp Gly Asp Asn
            180                 185                 190
Val Leu Leu Thr Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu
        195                 200                 205
Leu Tyr Leu Arg Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys
    210                 215                 220
Asn Leu Thr Gly Pro Gln Asn Ile Thr Leu Asn His Thr Asp Leu Val
225                 230                 235                 240
Pro Cys Leu Cys Ile Gln Val Trp Ser Leu Glu Pro Asp Ser Glu Arg
                245                 250                 255
Val Glu Phe Cys Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu
            260                 265                 270
Trp His Ile Ala Arg Leu Arg Val Leu Ser Pro Gly Val Trp Gln Leu
        275                 280                 285
Asp Ala Pro Cys Cys Leu Pro Gly Lys Val Thr Leu Cys Trp Gln Ala
    290                 295                 300
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```
Pro Asp Gln Ser Pro Cys Gln Pro Leu Val Pro Pro Val Pro Gln Lys
305                 310                 315                 320
Asn Ala Thr Val Asn Glu Pro Gln Asp Phe Gln Leu Val Ala Gly His
                325                 330                 335
Pro Asn Leu Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln
            340                 345                 350
Ala Cys Ser Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu
        355                 360                 365
Leu Val Glu Met Lys Thr Gly Leu Asn Asn Thr Ser Val Cys Ala Leu
    370                 375                 380
Glu Pro Ser Gly Cys Thr Pro Leu Pro Ser Met Ala Ser Thr Arg Ala
385                 390                 395                 400
Ala Arg Leu Gly Glu Glu Leu Leu Gln Asp Phe Arg Ser His Gln Cys
                405                 410                 415
Met Gln Leu Trp Asn Asp Asp Asn Met Gly Ser Leu Trp Ala Cys Pro
            420                 425                 430
Met Asp Lys Tyr Ile His Arg Arg Trp Val Leu Val Trp Leu Ala Cys
        435                 440                 445
Leu Leu Leu Ala Ala Ala Leu Phe Phe Phe Leu Leu Leu Lys Lys Asp
    450                 455                 460
Arg Arg Lys Ala Ala Arg Gly Ser Arg Thr Ala Leu Leu Leu His Ser
465                 470                 475                 480
Ala Asp Gly Ala Gly Tyr Glu Arg Leu Val Gly Ala Leu Ala Ser Ala
                485                 490                 495
Leu Ser Gln Met Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg
            500                 505                 510
Glu Leu Ser Ala His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg
        515                 520                 525
Arg Ile Leu Gln Glu Gly Gly Val Val Ile Leu Leu Phe Ser Pro Ala
    530                 535                 540
Ala Val Ala Gln Cys Gln Gln Trp Leu Gln Leu Gln Thr Val Glu Pro
545                 550                 555                 560
Gly Pro His Asp Ala Leu Ala Ala Trp Leu Ser Cys Val Leu Pro Asp
                565                 570                 575
Phe Leu Gln Gly Arg Ala Thr Gly Arg Tyr Val Gly Val Tyr Phe Asp
            580                 585                 590
Gly Leu Leu His Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro
        595                 600                 605
Leu Phe Ser Leu Pro Thr Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln
    610                 615                 620
Gly Gly Cys Ser Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg
625                 630                 635                 640
Val Thr Gln Ala Leu Arg Ser Ala Leu Asp Ser Cys Thr Ser Ser Ser
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Glu Ala Pro Gly Cys Cys Glu Glu Trp Asp Leu Gly Pro Cys Thr Thr
            660                 665                 670
Leu Glu
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<210> 3
<211> 2022
<212> DNA
<213> Artificial Sequence

<220>
<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> misc_feature
<222> (1)...(2022)
<223> n = A,T,C or G

<400> 3

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ytngarmgny tnatggarcc ncargayacn gcnmgntgyw snytnggnyt nwsntgycay     120
ytntgggayg gngaygtnyt ntgyytnccn ggnwsnytnc arwsngcncc nggnccngtn     180
ytngtnccna cnmgnytnca racngarytn gtnytnmgnt gyccncaraa racngaytgy     240
gcnytnmgng tnmgngtngt ngtncayytn gcngtncayg gncaytgggc ngarccngar     300
gargcnggna arwsngayws ngarytncar garwsnmgna aygcnwsnyt ncargcncar     360
gtngtnytnw snttycargc ntayccnath gcnmgntgyg cnytnytnga rgtncargtn     420
ccngcngayy tngtncarcc nggncarwsn gtnggnwsng cngtnttyga ytgyttygar     480
gcnwsnytng gngcngargt ncarathtgg wsntayacna arccnmgnta ycaraargar     540
ytnaayytna cncarcaryt nccngayggn gayaaygtny tnytnacnyt ngaygtnwsn     600
gargarcarg ayttywsntt yytnytntay ytnmgnccng tnccngaygc nytnaarwsn     660
ytntggtaya araayytnac nggnccncar aayathacny tnaaycayac ngayytngtn     720
ccntgyytnt gyathcargt ntggwsnytn garccngayw sngarmgngt ngarttytgy     780
ccnttymgng argayccngg ngcncaymgn aayytntggc ayathgcnmg nytnmgngtn     840
ytnwsnccng gngtntggca rytngaygcn ccntgytgyy tnccnggnaa rgtnacnytn     900
tgytggcarg cnccngayca rwsnccntgy carccnytng tnccnccngt nccncaraar     960
aaygcnacng tnaaygarcc ncargaytty carytngtng cnggncaycc naayytntgy    1020
gtncargtnw snacntggga raargtncar ytncargcnt gywsntgggc ngaywsnytn    1080
ggnccnttya argaygayat gytnytngtn garatgaara cnggnytnaa yaayacnwsn    1140
gtntgygcny tngarccnws nggntgyacn ccnytnccnw snatggcnws nacnmgngcn    1200
gcnmgnytng gngargaryt nytncargay ttymgnwsnc aycartgyat gcarytntgg    1260
aaygaygaya ayatgggnws nytntgggcn tgyccnatgg ayaartayat hcaymgnmgn    1320
tgggtnytng tntggytngc ntgyytnytn ytngcngcng cnytnttytt yttyytnytn    1380
ytnaaraarg aymgnmgnaa rgcngcnmgn ggnwsnmgna cngcnytnyt nytncaywsn    1440
gcngayggng cnggntayga rmgnytngtn ggngcnytng cnwsngcnyt nwsncaratg    1500
ccnytnmgng tngcngtnga yytntggwsn mgnmgngary tnwsngcnca yggngcnytn    1560
gcntggttyc aycaycarmg nmgnmgnath ytncargarg gnggngtngt nathytnytn    1620
ttywsnccng cngcngtngc ncartgycar cartggytnc arytncarac ngtngarccn    1680
ggnccncayg aygcnytngc ngcntggytn wsntgygtny tnccngaytt yytncarggn    1740
mgngcnacng gnmgntaygt nggngtntay ttygayggny tnytncaycc ngaywsngtn    1800
ccnwsnccnt tymgngtngc nccnytntty wsnytnccna cncarytncc ngcnttyytn    1860
gaygcnytnc arggnggntg ywsnacnwsn gcnggnmgnc cngcngaymg ngtngarmgn    1920
gtnacncarg cnytnmgnws ngcnytngay wsntgyacnw snwsnwsnga rgcnccnggn    1980
tgytgygarg artgggayyt nggnccntgy acnacnytng ar                       2022
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<210> 4
<211> 2328
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (197)...(2290)

<400> 4

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catggctgga gaggaattct agcccttgct ctctcccagg gacacggggc tgattgtcag     120
caggggcgag gggtctgccc ccccttgggg gggcaggacg gggcctcagg cctgggtgct     180
gtccggcacc tggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca ctg     232
                  Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu
                   1               5                  10

ggc cga aac cct gtg gtc gtc tct ctg gag aga ctg atg gag cct cag      280
Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln
         15                  20                  25

gac act gca cgc tgc tct cta ggc ctc tcc tgc cac ctc tgg gat ggt      328
Asp Thr Ala Arg Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly
     30                  35                  40

gac gtg ctc tgc ctg cct gga agc ctc cag tct gcc cca ggc cct gtg      376
```

```
Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val
 45                  50                  55                  60

cta gtg cct acc cgc ctg cag acg gag ctg gtg ctg agg tgt cca cag      424
Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln
                 65                  70                  75

aag aca gat tgc gcc ctc cgt gtc cgt gtg gtg gtc cac ttg gcc gtg      472
Lys Thr Asp Cys Ala Leu Arg Val Arg Val Val Val His Leu Ala Val
             80                  85                  90

cat ggg cac tgg gca gag cct gaa gaa gct gga aag tct gat tca gaa      520
His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu
         95                  100                 105

ctc cag gag tct agg aac gcc tct ctc cag gcc cag gtg gtg ctc tcc      568
Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
     110                 115                 120

ttc cag gcc tac ccc atc gcc cgc tgt gcc ctg ctg gag gtc cag gtg      616
Phe Gln Ala Tyr Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val
125                 130                 135                 140

ccc gct gac ctg gtg cag cct ggt cag tcc gtg ggt tct gcg gta ttt      664
Pro Ala Asp Leu Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe
                145                 150                 155

gac tgt ttc gag gct agt ctt ggg gct gag gta cag atc tgg tcc tac      712
Asp Cys Phe Glu Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr
            160                 165                 170

acg aag ccc agg tac cag aaa gag ctc aac ctc aca cag cag ctg cct      760
Thr Lys Pro Arg Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro
        175                 180                 185

gac tgc agg ggt ctt gaa gtc cgg gac agc atc cag agc tgc tgg gtc      808
Asp Cys Arg Gly Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp Val
    190                 195                 200

ctg ccc tgg ctc aat gtg tct aca gat ggt gac aat gtc ctt ctg aca      856
Leu Pro Trp Leu Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu Thr
205                 210                 215                 220

ctg gat gtc tct gag gag cag gac ttt agc ttc tta ctg tac ctg cgt      904
Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu Arg
                225                 230                 235

cca gtc ccg gat gct ctc aaa tcc ttg tgg tac aaa aac ctg act gga      952
Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr Gly
            240                 245                 250

cct cag aac att act tta aac cac aca gac ctg gtt ccc tgc ctc tgc     1000
Pro Gln Asn Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys
        255                 260                 265

att cag gtg tgg tcg cta gag cca gac tct gag agg gtc gaa ttc tgc     1048
Ile Gln Val Trp Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe Cys
    270                 275                 280

ccc ttc cgg gaa gat ccc ggt gca cac agg aac ctc tgg cac ata gcc     1096
```

```
Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu Trp His Ile Ala
285                 290                 295                 300

agg ctg cgg gta ctg tcc cca ggg gta tgg cag cta gat gcg cct tgc      1144
Arg Leu Arg Val Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro Cys
                305                 310                 315

tgt ctg ccg ggc aag gta aca ctg tgc tgg cag gca cca gac cag agt      1192
Cys Leu Pro Gly Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln Ser
            320                 325                 330

ccc tgc cag cca ctt gtg cca cca gtg ccc cag aag aac gcc act gtg      1240
Pro Cys Gln Pro Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr Val
        335                 340                 345

aat gag cca caa gat ttc cag ttg gtg gca ggc cac ccc aac ctc tgt      1288
Asn Glu Pro Gln Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu Cys
    350                 355                 360

gtc cag gtg agc acc tgg gag aag gtt cag ctg caa gcg tgc tcg tgg      1336
Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Ser Trp
365                 370                 375                 380

gct gac tcc ttg ggg ccc ttc aag gat gat atg ctg tta gtg gag atg      1384
Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu Met
                385                 390                 395

aaa acc ggc ctc aac aac aca tca gtc tgt gcc ttg gaa ccc agt ggc      1432
Lys Thr Gly Leu Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser Gly
            400                 405                 410

tgt aca cca ctg ccc agc atg gcc tcc acg aga gct gct cgc ctg gga      1480
Cys Thr Pro Leu Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu Gly
        415                 420                 425

gag gag ttg ctg caa gac ttc cga tca cac cag tgt atg cag ctg tgg      1528
Glu Glu Leu Leu Gln Asp Phe Arg Ser His Gln Cys Met Gln Leu Trp
    430                 435                 440

aac gat gac aac atg gga tcg cta tgg gcc tgc ccc atg gac aag tac      1576
Asn Asp Asp Asn Met Gly Ser Leu Trp Ala Cys Pro Met Asp Lys Tyr
445                 450                 455                 460

atc cac agg cgc tgg gtc cta gta tgg ctg gcc tgc cta ctc ttg gct      1624
Ile His Arg Arg Trp Val Leu Val Trp Leu Ala Cys Leu Leu Leu Ala
                465                 470                 475

gcg gcg ctt ttc ttc ttc ctc ctt cta aaa aag gac cgc agg aaa gcg      1672
Ala Ala Leu Phe Phe Phe Leu Leu Leu Lys Lys Asp Arg Arg Lys Ala
            480                 485                 490

gcc cgt ggc tcc cgc acg gcc ttg ctc ctc cac tcc gcc gac gga gcg      1720
Ala Arg Gly Ser Arg Thr Ala Leu Leu Leu His Ser Ala Asp Gly Ala
        495                 500                 505

ggc tac gag cgt ctg gtg gga gca ctg gcg tcc gcg ttg agc cag atg      1768
Gly Tyr Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Ser Gln Met
    510                 515                 520

cca ctg cgc gtg gcc gtg gac ctg tgg agc cgc cgc gag ctg agc gcg      1816
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Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala
525 530 535 540

cac gga gcc cta gcc tgg ttc cac cac cag cga cgc cgt atc ctg cag 1864
His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg Arg Ile Leu Gln
545 550 555

gag ggt ggc gtg gta atc ctt ctc ttc tcg ccc gcg gcc gtg gcg cag 1912
Glu Gly Gly Val Val Ile Leu Leu Phe Ser Pro Ala Ala Val Ala Gln
560 565 570

tgt cag cag tgg ctg cag ctc cag aca gtg gag ccc ggg ccg cat gac 1960
Cys Gln Gln Trp Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His Asp
575 580 585

gcc ctc gcc gcc tgg ctc agc tgc gtg cta ccc gat ttc ctg caa ggc 2008
Ala Leu Ala Ala Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly
590 595 600

cgg gcg acc ggc cgc tac gtc ggg gtc tac ttc gac ggg ctg ctg cac 2056
Arg Ala Thr Gly Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu His
605 610 615 620

cca gac tct gtg ccc tcc ccg ttc cgc gtc gcc ccg ctc ttc tcc ctg 2104
Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser Leu
625 630 635

ccc acg cag ctg ccg gct ttc ctg gat gca ctg cag gga ggc tgc tcc 2152
Pro Thr Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys Ser
640 645 650

act tcc gcg ggg cga ccc gcg gac cgg gtg gaa cga gtg acc cag gcg 2200
Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln Ala
655 660 665

ctg cgg tcc gcc ctg gac agc tgt act tct agc tcg gaa gcc cca ggc 2248
Leu Arg Ser Ala Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro Gly
670 675 680

tgc tgc gag gaa tgg gac ctg gga ccc tgc act aca cta gaa 2290
Cys Cys Glu Glu Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
685 690 695

taaaagccga tacagtattc ctaaaaaaaa aaaaaaaa 2328

<210> 5
<211> 698
<212> PRT
<213> mouse

<400> 5
Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Asn Pro
1 5 10 15
Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln Asp Thr Ala Arg
20 25 30
Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly Asp Val Leu Cys
35 40 45
Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val Leu Val Pro Thr
50 55 60
Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln Lys Thr Asp Cys
65 70 75 80

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Ala Leu Arg Val Arg Val Val Val His Leu Ala Val His Gly His Trp
                85                  90                  95
Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu Leu Gln Glu Ser
            100                 105                 110
Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr
        115                 120                 125
Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val Pro Ala Asp Leu
    130                 135                 140
Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe Asp Cys Phe Glu
145                 150                 155                 160
Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr Thr Lys Pro Arg
                165                 170                 175
Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro Asp Cys Arg Gly
            180                 185                 190
Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp Val Leu Pro Trp Leu
        195                 200                 205
Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu Thr Leu Asp Val Ser
    210                 215                 220
Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu Arg Pro Val Pro Asp
225                 230                 235                 240
Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr Gly Pro Gln Asn Ile
                245                 250                 255
Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp
            260                 265                 270
Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe Cys Pro Phe Arg Glu
        275                 280                 285
Asp Pro Gly Ala His Arg Asn Leu Trp His Ile Ala Arg Leu Arg Val
    290                 295                 300
Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro Cys Cys Leu Pro Gly
305                 310                 315                 320
Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln Ser Pro Cys Gln Pro
                325                 330                 335
Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr Val Asn Glu Pro Gln
            340                 345                 350
Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu Cys Val Gln Val Ser
        355                 360                 365
Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Ser Trp Ala Asp Ser Leu
    370                 375                 380
Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu Met Lys Thr Gly Leu
385                 390                 395                 400
Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser Gly Cys Thr Pro Leu
                405                 410                 415
Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu Glu Leu Leu
            420                 425                 430
Gln Asp Phe Arg Ser His Gln Cys Met Gln Leu Trp Asn Asp Asp Asn
        435                 440                 445
Met Gly Ser Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His Arg Arg
    450                 455                 460
Trp Val Leu Val Trp Leu Ala Cys Leu Leu Leu Ala Ala Ala Leu Phe
465                 470                 475                 480
Phe Phe Leu Leu Leu Lys Lys Asp Arg Arg Lys Ala Ala Arg Gly Ser
                485                 490                 495
Arg Thr Ala Leu Leu Leu His Ser Ala Asp Gly Ala Gly Tyr Glu Arg
            500                 505                 510
Leu Val Gly Ala Leu Ala Ser Ala Leu Ser Gln Met Pro Leu Arg Val
        515                 520                 525
Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala His Gly Ala Leu
    530                 535                 540
Ala Trp Phe His His Gln Arg Arg Arg Ile Leu Gln Glu Gly Gly Val
545                 550                 555                 560
Val Ile Leu Leu Phe Ser Pro Ala Ala Val Ala Gln Cys Gln Gln Trp
                565                 570                 575
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Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His Asp Ala Leu Ala Ala
            580                 585                 590
Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala Thr Gly
        595                 600                 605
Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu His Pro Asp Ser Val
    610                 615                 620
Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser Leu Pro Thr Gln Leu
625                 630                 635                 640
Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys Ser Thr Ser Ala Gly
                645                 650                 655
Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln Ala Leu Arg Ser Ala
            660                 665                 670
Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro Gly Cys Cys Glu Glu
        675                 680                 685
Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
    690                 695
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<210> 6
<211> 2094
<212> DNA
<213> Artificial Sequence

<220>
<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:5.

<221> misc_feature
<222> (1)...(2094)
<223> n = A,T,C or G

<400> 6

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ytngarmgny tnatggarcc ncargayacn gcnmgntgyw snytnggnyt nwsntgycay     120
ytntgggayg gngaygtnyt ntgyytnccn ggnwsnytnc arwsngcncc nggnccngtn     180
ytngtnccna cnmgnytnca racngarytn gtnytnmgnt gyccncaraa racngaytgy     240
gcnytnmgng tnmgngtngt ngtncayytn gcngtncayg gncaytgggc ngarccngar     300
gargcnggna arwsngayws ngarytncar garwsnmgna aygcnwsnyt ncargcncar     360
gtngtnytnw snttycargc ntayccnath gcnmgntgyg cnytnytnga rgtncargtn     420
ccngcngayy tngtncarcc nggncarwsn gtnggnwsng cngtnttyga ytgyttygar     480
gcnwsnytng gngcngargt ncarathtgg wsntayacna arccnmgnta ycaraargar     540
ytnaayytna cncarcaryt nccngaytgy mgnggnytng argtnmgnga ywsnathcar     600
wsntgytggg tnytnccntg gytnaaygtn wsnacngayg gngayaaygt nytnytnacn     660
ytngaygtnw sngargarca rgayttywsn ttyytnytnt ayytnmgncc ngtnccngay     720
gcnytnaarw snytntggta yaaraayytn acnggnccnc araayathac nytnaaycay     780
acngayytng tnccntgyyt ntgyathcar gtntggwsny tngarccnga ywsngarmgn     840
gtngarttyt gyccnttymg ngargayccn ggngcncaym gnaayytntg gcayathgcn     900
mgnytnmgng tnytnwsncc nggngtntgg carytngayg cnccntgytg yytnccnggn     960
aargtnacny tntgytggca rgcnccngay carwsnccnt gycarccnyt ngtnccnccn    1020
gtnccncara araaygcnac ngtnaaygar ccncargayt tycarytngt ngcnggncay    1080
ccnaayytnt gygtncargt nwsnacntgg garaargtnc arytncargc ntgywsntgg    1140
gcngaywsny tnggnccntt yaargaygay atgytnytng tngaratgaa racnggnytn    1200
aayaayacnw sngtntgygc nytngarccn wsnggntgya cnccnytncc nwsnatggcn    1260
wsnacnmgng cngcnmgnyt nggngargar ytnytncarg ayttymgnws ncaycartgy    1320
atgcarytnt ggaaygayga yaayatgggn wsnytntggg cntgyccnat ggayaartay    1380
athcaymgnm gntgggtnyt ngtntggytn gcntgyytny tnytngcngc ngcnytntty    1440
ttyttyytny tnytnaaraa rgaymgnmgn aargcngcnm gnggnwsnmg nacngcnytn    1500
ytnytncayw sngcngaygg ngcnggntay garmgnytng tnggngcnyt ngcnwsngcn    1560
ytnwsncara tgccnytnmg ngtngcngtn gayytntggw snmgnmgnga rytnwsngcn    1620
cayggngcny tngcntggtt ycaycaycar mgnmgnmgna thytncarga rggnggngtn    1680
gtnathytny tnttywsncc ngcngcngtn gcncartgyc arcartggyt ncarytncar    1740
acngtngarc cnggnccnca ygaygcnytn gcngcntggy tnwsntgygt nytnccngay    1800
ttyytncarg gnmgngcnac nggnmgntay gtnggngtnt ayttygaygg nytnytncay    1860
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ccngaywsng tnccnwsncc nttymgngtn gcnccnytnt tywsnytncc nacncarytn 1920
ccngcnttyy tngaygcnyt ncarggnggn tgywsnacnw sngcnggnmg nccngcngay 1980
mgngtngarm gngtnacnca rgcnytnmgn wsngcnytng aywsntgyac nwsnwsnwsn 2040
gargcnccng gntgytgyga rgartgggay ytnggnccnt gyacnacnyt ngar 2094

<210> 7
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 7
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1 5 10 15

<210> 8
<211> 692
<212> PRT
<213> Human

<400> 8
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Val Val Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
20 25 30
Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
35 40 45
Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
50 55 60
His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
65 70 75 80
Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
85 90 95
Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly
100 105 110
Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
115 120 125
Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
130 135 140
Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
145 150 155 160
Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
165 170 175
Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
180 185 190
Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu
195 200 205
Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp
210 215 220
Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr
225 230 235 240
Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu
245 250 255
Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile
260 265 270
Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala
275 280 285
Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro
290 295 300

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Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly
305                 310                 315                 320
Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr
                325                 330                 335
Val Asp Lys Val Leu Glu Phe Pro Leu Leu Lys Gly His Pro Asn Leu
            340                 345                 350
Cys Val Gln Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu
        355                 360                 365
Trp Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu
    370                 375                 380
Thr Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser
385                 390                 395                 400
Gly Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu
                405                 410                 415
Gly Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu
            420                 425                 430
Trp Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr
        435                 440                 445
Ile His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala
    450                 455                 460
Ala Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Ala
465                 470                 475                 480
Ala Ala Arg Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser
                485                 490                 495
Gly Phe Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu
            500                 505                 510
Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala
        515                 520                 525
Gln Gly Pro Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln
    530                 535                 540
Glu Gly Gly Val Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu
545                 550                 555                 560
Cys Ser Glu Trp Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly
                565                 570                 575
Pro His Asp Ala Phe Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe
            580                 585                 590
Leu Gln Gly Arg Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg
        595                 600                 605
Leu Leu His Pro Asp Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val
    610                 615                 620
Phe Thr Leu Pro Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln
625                 630                 635                 640
Pro Arg Ala Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val
                645                 650                 655
Ser Arg Ala Leu Gln Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly
            660                 665                 670
Thr Pro Ala Pro Gly Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala
        675                 680                 685
Gly Asp Gly Thr
    690
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